

SEQUENCE LISTING

<110> Medlock, Eugene
Yeh, Richard
Silbiger, Scott M.
Elliot, Gary S.
Nguyen, Hung Q.
Jing, Shugian

<120> IL-17 Like Molecules and Uses Thereof

<130> 01017/37128C

<140>

<141>

<150> 09/886,404

<151> 2001-06-21

<150> 09/810,384

<151> 2001-03-16

<150> 60/266,159

<151> 2001-02-02

<150> 60/213,125

<151> 2000-06-22

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 644

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (159)..(641)

<400> 1

ctcaagtcac tccctaaaaa gacagtggaa ataaatttga ataaacaaaa caggcttgct 60

gaaaataaaa tcaggactcc taacctgctc cagtcagcct gcttccacga ggctgtcag 120

tcagtgtccc acttgtgact gagtgtgcag tgcccagc atg tac cag gtg gtt gca 176
Met Tyr Gln Val Val Ala

1

5

ttc ttg gca atg gtc atg gga acc cac acc tac agc cac tgg ccc agc 224
Phe Leu Ala Met Val Met Gly Thr His Thr Tyr Ser His Trp Pro Ser
10 15 20

tgc tgc ccc agc aaa ggg cag gac acc tct gag gag ctg ctg agg tgg 272
Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser Glu Glu Leu Leu Arg Trp
25 30 35

agc act gtg cct gtg cct ccc cta gag cct gct agg ccc aac cgc cac 320
Ser Thr Val Pro Val Pro Pro Leu Glu Pro Ala Arg Pro Asn Arg His
40 45 50

cca gag tcc tgt agg gcc agt gaa gat gga ccc ctc aac agc agg gcc 368
Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala
55 60 65 70

atc tcc ccc tgg aga tat gag ttg gac aga gac ttg aac cgg ctc ccc 416
Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro
75 80 85

cag gac ctg tac cac gcc cgt tgc ctg tgc ccg cac tgc gtc agc cta 464
Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu
90 95 100

cag aca ggc tcc cac atg gac ccc cgg ggc aac tcg gag ctg ctc tac 512
Gln Thr Gly Ser His Met Asp Pro Arg Gly Asn Ser Glu Leu Leu Tyr
105 110 115

cac aac cag act gtc ttc tac cgg cgg cca tgc cat ggc gag aag ggc 560
His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly
120 125 130

acc cac aag ggc tac tgc ctg gag cgc agg ctg tac cgt gtt tcc tta 608
Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu
135 140 145 150

gct tgt gtg tgt gtg cgg ccc cgt gtg atg ggc tag 644
Ala Cys Val Cys Val Arg Pro Arg Val Met Gly
155 160

<210> 2

<211> 161

<212> PRT

<213> Homo sapiens

<400> 2

Met Tyr Gln Val Val Ala Phe Leu Ala Met Val Met Gly Thr His Thr
1 5 10 15

Tyr Ser His Trp Pro Ser Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser
20 25 30

Glu Glu Leu Leu Arg Trp Ser Thr Val Pro Val Pro Pro Leu Glu Pro
35 40 45

Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly
50 55 60

Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg
65 70 75 80

Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys
85 90 95

Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly
100 105 110

Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro
115 120 125

Cys His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg
130 135 140

Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met
145 150 155 160

Gly

<210> 3
<211> 1013
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(507)

<400> 3
atg tac cag gct gtt gca ttc ttg gca atg atc gtg gga acc cac acc 48
Met Tyr Gln Ala Val Ala Phe Leu Ala Met Ile Val Gly Thr His Thr
1 5 10 15
gtc agc ttg cgg atc cag gag ggc tgc agt cac ttg ccc agc tgc tgc 96
Val Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys
20 25 30
ccc agc aaa gag caa gaa ccc ccg gag gag tgg ctg aag tgg agc tct 144
Pro Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser
35 40 45
gca tct gtg tcc ccc cca gag cct ctg agc cac acc cac cac gca gaa 192
Ala Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu
50 55 60
tcc tgc agg gcc agc aag gat ggc ccc ctc aac agc agg gcc atc tct 240
Ser Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser
65 70 75 80
cct tgg agc tat gag ttg gac agg gac ttg aat cgg gtc ccc cag gac 288
Pro Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp
85 90 95
ctg tac cac gct cga tgc ctg tgc cca cac tgc gtc agc cta cag aca 336
Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr
100 105 110
ggc tcc cac atg gac ccg ctg ggc aac tcc gtc cca ctt tac cac aac 384
Gly Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn
115 120 125
cag acg gtc ttc tac cgg cgg cca tgc cat ggc gag gaa ggt acc cat 432
Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His
130 135 140
cgc cgc tac tgc ttg gag cgc agg ctc tac cga gtc tcc ttg gct tgt 480
Arg Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys
145 150 155 160
gtg tgt gtg cgg ccc cgg gtc atg gct tagtcatgct caccacctgc 527
Val Cys Val Arg Pro Arg Val Met Ala
165
ctgaggctga tgcccggttg ggagagaggg ccaggtgtac aatcaccttg ccaatgcggg 587
ccgggttcaa gccctccaaa gccctacctg aagcagcagg ctcccgggac aagatggagg 647

```

acttggggag aaactctgac ttttgcaactt tttggaagca cttttgggaa ggagcagggtt 707
ccgcttgtgc tgctagagga tgctgttggtg gcattttctac tcaggaacgg actccaaagg 767
cctgotgacc ctggaagcca tactcctggc tcccttcccc tgaatcccc aactcctggc 827
acaggcactt tctccacctc tccccctttg ccttttggtg tgtttgtttg tgcattgcca 887
ctctgcgtgc agccagggtg aattgccttg aaggatgggt ctgaggtgaa agctgttatc 947
gaaagtgaag agatttatcc aaataaacat ctgtgtttta aaaaaaaaaa aaaaaaaaaa 1007
aaaaaa 1013

```

<210> 4
 <211> 169
 <212> PRT
 <213> Mus musculus

<400> 4

Met	Tyr	Gln	Ala	Val	Ala	Phe	Leu	Ala	Met	Ile	Val	Gly	Thr	His	Thr
1				5					10					15	
Val	Ser	Leu	Arg	Ile	Gln	Glu	Gly	Cys	Ser	His	Leu	Pro	Ser	Cys	Cys
			20					25					30		
Pro	Ser	Lys	Glu	Gln	Glu	Pro	Pro	Glu	Glu	Trp	Leu	Lys	Trp	Ser	Ser
		35					40					45			
Ala	Ser	Val	Ser	Pro	Pro	Glu	Pro	Leu	Ser	His	Thr	His	His	Ala	Glu
		50				55					60				
Ser	Cys	Arg	Ala	Ser	Lys	Asp	Gly	Pro	Leu	Asn	Ser	Arg	Ala	Ile	Ser
	65				70					75					80
Pro	Trp	Ser	Tyr	Glu	Leu	Asp	Arg	Asp	Leu	Asn	Arg	Val	Pro	Gln	Asp
			85						90					95	
Leu	Tyr	His	Ala	Arg	Cys	Leu	Cys	Pro	His	Cys	Val	Ser	Leu	Gln	Thr
			100					105					110		
Gly	Ser	His	Met	Asp	Pro	Leu	Gly	Asn	Ser	Val	Pro	Leu	Tyr	His	Asn
		115					120					125			
Gln	Thr	Val	Phe	Tyr	Arg	Arg	Pro	Cys	His	Gly	Glu	Glu	Gly	Thr	His
		130				135					140				
Arg	Arg	Tyr	Cys	Leu	Glu	Arg	Arg	Leu	Tyr	Arg	Val	Ser	Leu	Ala	Cys
	145				150					155					160
Val	Cys	Val	Arg	Pro	Arg	Val	Met	Ala							
					165										

<210> 5
 <211> 155
 <212> PRT
 <213> Homo sapiens

<400> 5

Met	Thr	Pro	Gly	Lys	Thr	Ser	Leu	Val	Ser	Leu	Leu	Leu	Leu	Leu	Ser
1				5					10					15	

Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly
20 25 30

Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
35 40 45

Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
50 55 60

Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
65 70 75 80

Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
85 90 95

Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
100 105 110

Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
115 120 125

Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
130 135 140

Thr Cys Val Thr Pro Ile Val His His Val Ala
145 150 155

<210> 6

<211> 117

<212> PRT

<213> Homo sapiens

<400> 6

Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu
1 5 10 15

Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys
20 25 30

Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg
35 40 45

Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val
50 55 60

Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val
65 70 75 80

Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg
85 90 95

Thr Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Val Ala Gly
100 105 110

Cys Thr Cys Ile Phe
115

<210> 7

<211> 117

<212> PRT

<213> Homo sapiens

<400> 7

Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu
1 5 10 15

Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys
20 25 30

Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg
35 40 45

Ile Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val
50 55 60

Asn Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val
65 70 75 80

Phe Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg
85 90 95

Thr Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly
100 105 110

Cys Thr Cys Ile Phe
115

<210> 8

<211> 197

<212> PRT

<213> Homo sapiens

<400> 8

Met Thr Leu Leu Pro Gly Leu Leu Phe Leu Thr Trp Leu His Thr Cys
1 5 10 15

Leu Ala His His Asp Pro Ser Leu Arg Gly His Pro His Ser His Gly
20 25 30

Thr Pro His Cys Tyr Ser Ala Glu Glu Leu Pro Leu Gly Gln Ala Pro
35 40 45

Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln Ala Leu Pro Val
50 55 60

Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His Arg Gly Arg His Glu
65 70 75 80

Arg Pro Ser Ala Thr Thr Gln Cys Pro Val Leu Arg Pro Glu Glu Val
85 90 95

Leu Glu Ala Asp Thr His Gln Arg Ser Ile Ser Pro Trp Arg Tyr Arg
100 105 110

Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe Ala Glu
115 120 125

Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu Thr Ala
130 135 140

Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu Arg Arg
 145 150 155 160
 Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe
 165 170 175
 Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val
 180 185 190
 Leu Pro Arg Ser Val
 195

<210> 9
 <211> 1496
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (511)..(987)

<400> 9
 ccgggcaggt gccctcggcg cgtcccaaag cttagggaag ctccaggtgt cttgggaaat 60
 gaagaaaaag gccaccgagc aaaaaggaac agagaagggg aggagcagtg ctgtgggctc 120
 gcctaggggtc gagggccatt atcacctaca aatcagaatg tgggagtgct attctagagg 180
 tctccatctt tgccattgct gggtcgctca gaaaagtgtg atggggttgt cccattgccca 240
 agaacagctt ctgcttacca gcaggtgctg acctctttcc ccagaggcac agggaaggaa 300
 ttccagcccc ggttggtgc cagaggcttc ctctggcggt gggtagagag gcagagaaaag 360
 aaaccccaaa tgtctctat gaaaaacaat gtccccgtca tccagggcag atcattctgc 420
 agtgtcaaca gttgagacaa gaagctgggg tcattttctg tgccaaagag tgccgtttct 480
 gcactggcca aggctgttgc attcttggca atg atc gtg gga acc cac acc gtc 534
 Met Ile Val Gly Thr His Thr Val
 1 5
 agc ttg cgg atc cag gag ggc tgc agt cac ttg ccc agc tgc tgc ccc 582
 Ser Leu Arg Ile Gln Glu Gly Cys Ser His Leu Pro Ser Cys Cys Pro
 10 15 20
 agc aaa gag caa gaa ccc ccg gag gag tgg ctg aag tgg agc tct gca 630
 Ser Lys Glu Gln Glu Pro Pro Glu Glu Trp Leu Lys Trp Ser Ser Ala
 25 30 35 40
 tct gtg tcc ccc cca gag cct ctg agc cac acc cac cac gca gaa tcc 678
 Ser Val Ser Pro Pro Glu Pro Leu Ser His Thr His His Ala Glu Ser
 45 50 55
 tgc agg gcc agc aag gat ggc ccc ctc aac agc agg gcc atc tct cct 726
 Cys Arg Ala Ser Lys Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser Pro
 60 65 70
 tgg agc tat gag ttg gac agg gac ttg aat cgg gtc ccc cag gac ctg 774
 Trp Ser Tyr Glu Leu Asp Arg Asp Leu Asn Arg Val Pro Gln Asp Leu
 75 80 85

tac cac gct cga tgc ctg tgc cca cac tgc gtc agc cta cag aca ggc 822
Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr Gly
90 95 100

tcc cac atg gac ccg ctg ggc aac tcc gtc cca ctt tac cac aac cag 870
Ser His Met Asp Pro Leu Gly Asn Ser Val Pro Leu Tyr His Asn Gln
105 110 115 120

acg gtc ttc tac cgg cgg cca tgc cat ggc gag gaa ggt acc cat cgc 918
Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Glu Gly Thr His Arg
125 130 135

cgc tac tgc ttg gag cgc agg ctc tac cga gtc tcc ttg gct tgt gtg 966
Arg Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu Ala Cys Val
140 145 150

tgt gtg cgg ccc cgg gtc atg gcttagtcat gctcaccacc tgcttgaggc 1017
Cys Val Arg Pro Arg Val Met
155

tgatgccccg ttgggagaga gggccaggtg tacaatcacc ttgccaatgc gggccgggtt 1077

caagccctcc aaagccctac ctgaagcagc aggcctcccg gacaagatgg aggacttggg 1137

gagaaactct gacttttgca ctttttgga gcaacttttg gaaggagcag gttccgcttg 1197

tgctgctaga ggatgctgtt gtggcatttc tactcaggaa cggactccaa aggcctgctg 1257

accttggaag ccatactcct ggctcctttc ccctgaatcc cccaactcct ggcacaggca 1317

ctttctccac ctctccccct ttgccttttg ttgtgtttgt ttgtgcatgc caactctgcg 1377

tgcagccagg tgtaattgcc ttgaaggatg gttctgaggt gaaagctggt atcgaaagtg 1437

aagagattta tccaaataaa catctgtgtt taaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1496

<210> 10
<211> 159
<212> PRT
<213> Mus musculus

<400> 10
Met Ile Val Gly Thr His Thr Val Ser Leu Arg Ile Gln Glu Gly Cys
1 5 10 15

Ser His Leu Pro Ser Cys Cys Pro Ser Lys Glu Gln Glu Pro Pro Glu
20 25 30

Glu Trp Leu Lys Trp Ser Ser Ala Ser Val Ser Pro Pro Glu Pro Leu
35 40 45

Ser His Thr His His Ala Glu Ser Cys Arg Ala Ser Lys Asp Gly Pro
50 55 60

Leu Asn Ser Arg Ala Ile Ser Pro Trp Ser Tyr Glu Leu Asp Arg Asp
65 70 75 80

Leu Asn Arg Val Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro
85 90 95

His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Leu Gly Asn
100 105 110

Ser Val Pro Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys
115 120 125

His Gly Glu Glu Gly Thr His Arg Arg Tyr Cys Leu Glu Arg Arg Leu
130 135 140

Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met
145 150 155

<210> 11

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epogen signal
peptide

<400> 11

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly
20 25

<210> 12

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide of Fc
fragment

<400> 12

Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 13

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide of HIV
TAT protein

<400> 13

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg
1 5 10

<210> 14

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide of HIV
TAT protein

<400> 14

Phe Ile Thr Cys Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln
1 5 10 15

Arg Arg Arg

<210> 15

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

```

<400> 15
tagggccagt gaagatgg 18

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 16
tacagcctgc gctccaggca gtagcc 26

<210> 17
<211> 1841
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (50)..(1555)

<400> 17
ataaaaagcgc agcgtgcggg tggcctggat cccgcgcagt ggcccggcg atg tcg ctc 58
                                     Met Ser Leu
                                     1

gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc gta ccc cga gag 106
Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
      5                      10                      15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154
Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
      20                      25                      30                      35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202
Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
                      40                      45                      50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250
Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
                      55                      60                      65

gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298
Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
      70                      75                      80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346
Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser Tyr Ser Cys
      85                      90                      95

gtg agg tgc aat tac aca gag gcc ttc cag act cag acc aga ccc tct 394
Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr Arg Pro Ser
      100                      105                      110                      115

ggg ggt aaa tgg aca ttt tcc tac atc ggc ttc cct gta gag ctg aac 442
Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn
      120                      125                      130

```

aca gtc tat ttc att ggg gcc cat aat att cct aat gca aat atg aat	490
Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn	
135 140 145	
gaa gat ggc cct tcc atg tct gtg aat ttc acc tca cca ggc tgc cta	538
Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu	
150 155 160	
gac cac ata atg aaa tat aaa aaa aag tgt gtc aag gcc gga agc ctg	586
Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu	
165 170 175	
tgg gat ccg aac atc act gct tgt aag aag aat gag gag aca gta gaa	634
Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu	
180 185 190 195	
gtg aac ttc aca acc act ccc ctg gga aac aga tac atg gct ctt atc	682
Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile	
200 205 210	
caa cac agc act atc atc ggg ttt tct cag gtg ttt gag cca cac cag	730
Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln	
215 220 225	
aag aaa caa acg cga gct tca gtg gtg att cca gtg act ggg gat agt	778
Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser	
230 235 240	
gaa ggt gct acg gtg cag ctg act cca tat ttt cct act tgt ggc agc	826
Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser	
245 250 255	
gac tgc atc cga cat aaa gga aca gtt gtg ctc tgc cca caa aca ggc	874
Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly	
260 265 270 275	
gtc cct ttc cct ctg gat aac aac aaa agc aag ccg gga ggc tgg ctg	922
Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu	
280 285 290	
cct ctc ctc ctg ctg tct ctg ctg gtg gcc aca tgg gtg ctg gtg gca	970
Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala	
295 300 305	
ggg atc tat cta atg tgg agg cac gaa agg atc aag aag act tcc ttt	1018
Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe	
310 315 320	
tct acc acc aca cta ctg ccc ccc att aag gtt ctt gtg gtt tac cca	1066
Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro	
325 330 335	
tct gaa ata tgt ttc cat cac aca att tgt tac ttc act gaa ttt ctt	1114
Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu	
340 345 350 355	
caa aac cat tgc aga agt gag gtc atc ctc gaa aag tgg cag aaa aag	1162
Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys	
360 365 370	

```

aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc act caa aag aag 1210
Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys
375 380 385

gca gca gac aaa gtc gtc ttc ctt ctt tcc aat gac gtc aac agt gtg 1258
Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val
390 395 400

tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc agt gag aac tct 1306
Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser
405 410 415

caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc agt gat cta aga 1354
Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg
420 425 430 435

agc cag att cat ctg cac aaa tac gtg gtg gtc tac ttt aga gag att 1402
Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile
440 445 450

gat aca aaa gac gat tac aat gct ctc agt gtc tgc ccc aag tac cac 1450
Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His
455 460 465

ctc atg aag gat gcc act gct ttc tgt gca gaa ctt ctc cat gtc aag 1498
Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys
470 475 480

cag cag gtg tca gca gga aaa aga tca caa gcc tgc cac gat ggc tgc 1546
Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys
485 490 495

tgc tcc ttg tagccacccc atgagaagca agagacctta aaggcttctt 1595
Cys Ser Leu
500

atcccaccaa ttacagggaa aaaacgtgtg atgacctga agcttactat gcagcctaca 1655

aacagcctta gtaattaaaa cattttatac caataaaaatt ttcaaataatt gctaactaat 1715

gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt tatacataga 1775

aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca ataaagcatc 1835

ttcagc 1841

<210> 18
<211> 502
<212> PRT
<213> Homo sapiens

<400> 18
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

```

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
100 105 110

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
115 120 125

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
130 135 140

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
145 150 155 160

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
165 170 175

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
180 185 190

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
195 200 205

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
210 215 220

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
225 230 235 240

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
245 250 255

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
260 265 270

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
275 280 285

Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
290 295 300

Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
305 310 315 320

Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
325 330 335

Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
340 345 350

Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
355 360 365

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
370 375 380

Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
385 390 395 400

Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
405 410 415

Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
420 425 430

Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
435 440 445

Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
450 455 460

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
465 470 475 480

His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
485 490 495

Asp Gly Cys Cys Ser Leu
500

<210> 19

<211> 2015

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1729)

<400> 19

ataaaagcgc agcgtgcggg tggcctggat cccgcgcagt ggcccggcg atg tcg ctc 58
Met Ser Leu
1

gtg ctg cta agc ctg gcc gcg ctg tgc agg agc gcc gta ccc cga gag 106
Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val Pro Arg Glu
5 10 15

ccg acc gtt caa tgt ggc tct gaa act ggg cca tct cca gag tgg atg 154
Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro Glu Trp Met
20 25 30 35

cta caa cat gat cta atc ccc gga gac ttg agg gac ctc cga gta gaa 202
Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu Arg Val Glu
40 45 50

cct gtt aca act agt gtt gca aca ggg gac tat tca att ttg atg aat 250
Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile Leu Met Asn
55 60 65

gta agc tgg gta ctc cgg gca gat gcc agc atc cgc ttg ttg aag gcc 298
Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu Leu Lys Ala
70 75 80

acc aag att tgt gtg acg ggc aaa agc aac ttc cag tcc tac agc tgt 346

Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser	Tyr	Ser	Cys		
	85					90					95						
gtg	agg	ctg	gag	tgc	agt	ggg	gcg	atc	atg	gct	cgc	tgc	gac	ctc	aat	394	
Val	Arg	Leu	Glu	Cys	Ser	Gly	Ala	Ile	Met	Ala	Arg	Cys	Asp	Leu	Asn		
100					105					110					115		
ctt	ctg	ggc	tca	agc	gat	cgt	tct	gct	tca	gcc	tcc	cga	gcg	gct	ggg	442	
Leu	Leu	Gly	Ser	Ser	Asp	Arg	Ser	Ala	Ser	Ala	Ser	Arg	Ala	Ala	Gly		
				120					125						130		
act	gca	ggc	gtg	ggc	cac	cag	acc	tgg	cta	att	ttt	gta	gtt	ttt	gta	490	
Thr	Ala	Gly	Val	Gly	His	Gln	Thr	Trp	Leu	Ile	Phe	Val	Val	Phe	Val		
			135					140						145			
gag	ggg	ggg	ttc	acc	gtg	ttg	ctg	gtc	ttg	aat	tcc	agt	gct	cag	gcg	538	
Glu	Gly	Gly	Phe	Thr	Val	Leu	Leu	Val	Leu	Asn	Ser	Ser	Ala	Gln	Ala		
		150					155					160					
atc	tgc	ctg	cct	cgg	ctt	ccc	aaa	gtg	ctg	gga	tta	cag	tgg	aca	ttt	586	
Ile	Cys	Leu	Pro	Arg	Leu	Pro	Lys	Val	Leu	Gly	Leu	Gln	Trp	Thr	Phe		
		165				170					175						
tcc	tac	atc	ggc	ttc	cct	gta	gag	ctg	aac	aca	gtc	tat	ttc	att	ggg	634	
Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn	Thr	Val	Tyr	Phe	Ile	Gly		
180					185					190					195		
gcc	cat	aat	att	cct	aat	gca	aat	atg	aat	gaa	gat	ggc	cct	tcc	atg	682	
Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp	Gly	Pro	Ser	Met		
				200					205						210		
tct	gtg	aat	ttc	acc	tca	cca	ggc	tgc	cta	gac	cac	ata	atg	aaa	tat	730	
Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asp	His	Ile	Met	Lys	Tyr		
			215					220						225			
aaa	aaa	aag	tgt	gtc	aag	gcc	gga	agc	ctg	tgg	gat	ccg	aac	atc	act	778	
Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr		
		230					235					240					
gct	tgt	aag	aag	aat	gag	gag	aca	gta	gaa	gtg	aac	ttc	aca	acc	act	826	
Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	Val	Asn	Phe	Thr	Thr	Thr		
		245				250					255						
ccc	ctg	gga	aac	aga	tac	atg	gct	ctt	atc	caa	cac	agc	act	atc	atc	874	
Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	Gln	His	Ser	Thr	Ile	Ile		
260					265					270					275		
ggg	ttt	tct	cag	gtg	ttt	gag	cca	cac	cag	aag	aaa	caa	acg	cga	gct	922	
Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln	Lys	Lys	Gln	Thr	Arg	Ala		
				280					285						290		
tca	gtg	gtg	att	cca	gtg	act	ggg	gat	agt	gaa	ggg	gct	acg	gtg	cag	970	
Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln		
			295					300						305			
ctg	act	cca	tat	ttt	cct	act	tgt	ggc	agc	gac	tgc	atc	cga	cat	aaa	1018	
Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys		
		310					315						320				
gga	aca	gtt	gtg	ctc	tgc	cca	caa	aca	ggc	gtc	cct	ttc	cct	ctg	gat	1066	
Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp		
		325				330					335						

aac aac aaa agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct	1114
Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser	
340 345 350 355	
ctg ctg gtg gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg	1162
Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp	
360 365 370	
agg cac gaa agg atc aag aag act tcc ttt tct acc acc aca cta ctg	1210
Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu	
375 380 385	
ccc ccc att aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat	1258
Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His	
390 395 400	
cac aca att tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt	1306
His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser	
405 410 415	
gag gtc atc ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt	1354
Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly	
420 425 430 435	
cca gtg cag tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc	1402
Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val	
440 445 450	
ttc ctt ctt tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc	1450
Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly	
455 460 465	
aag agc gag ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt	1498
Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu	
470 475 480	
gcc ttt aac ctt ttc tgc agt gat cta aga agc cag att cat ctg cac	1546
Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His	
485 490 495	
aaa tac gtg gtg gtc tac ttt aga gag att gat aca aaa gac gat tac	1594
Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr	
500 505 510 515	
aat gct ctc agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act	1642
Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr	
520 525 530	
gct ttc tgt gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga	1690
Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly	
535 540 545	
aaa aga tca caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccacccc	1739
Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu	
550 555 560	
atgagaagca agagacctta aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg	1799
atgatcctga agcttactat gcagcctaca aacagcctta gtaattaaaa cattttatac	1859
caataaaatt ttcaaattatt gctaactaat gtagcattaa ctaacgattg gaaactacat	1919

```
<210> 20
<211> 560
<212> PRT
<213> Homo sapiens
```

<400>	20															
Met	Ser	Leu	Val	Leu	Leu	Ser	Leu	Ala	Ala	Leu	Cys	Arg	Ser	Ala	Val	
1				5					10					15		
Pro	Arg	Glu	Pro	Thr	Val	Gln	Cys	Gly	Ser	Glu	Thr	Gly	Pro	Ser	Pro	
			20					25					30			
Glu	Trp	Met	Leu	Gln	His	Asp	Leu	Ile	Pro	Gly	Asp	Leu	Arg	Asp	Leu	
		35					40					45				
Arg	Val	Glu	Pro	Val	Thr	Thr	Ser	Val	Ala	Thr	Gly	Asp	Tyr	Ser	Ile	
	50					55					60					
Leu	Met	Asn	Val	Ser	Trp	Val	Leu	Arg	Ala	Asp	Ala	Ser	Ile	Arg	Leu	
65					70					75					80	
Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser	
				85					90					95		
Tyr	Ser	Cys	Val	Arg	Leu	Glu	Cys	Ser	Gly	Ala	Ile	Met	Ala	Arg	Cys	
			100					105					110			
Asp	Leu	Asn	Leu	Leu	Gly	Ser	Ser	Asp	Arg	Ser	Ala	Ser	Ala	Ser	Arg	
		115					120					125				
Ala	Ala	Gly	Thr	Ala	Gly	Val	Gly	His	Gln	Thr	Trp	Leu	Ile	Phe	Val	
	130					135					140					
Val	Phe	Val	Glu	Gly	Gly	Phe	Thr	Val	Leu	Leu	Val	Leu	Asn	Ser	Ser	
145					150					155					160	
Ala	Gln	Ala	Ile	Cys	Leu	Pro	Arg	Leu	Pro	Lys	Val	Leu	Gly	Leu	Gln	
				165					170					175		
Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn	Thr	Val	Tyr	
			180					185					190			
Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp	Gly	
		195					200					205				
Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asp	His	Ile	
	210					215					220					
Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	Trp	Asp	Pro	
225					230					235					240	
Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	Val	Asn	Phe	
				245					250					255		
Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	Gln	His	Ser	
			260					265					270			

Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
275 280 285

Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
290 295 300

Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
305 310 315 320

Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
325 330 335

Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu
340 345 350

Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr
355 360 365

Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr
370 375 380

Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile
385 390 395 400

Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His
405 410 415

Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala
420 425 430

Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp
435 440 445

Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly
450 455 460

Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu
465 470 475 480

Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile
485 490 495

His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys
500 505 510

Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys
515 520 525

Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val
530 535 540

Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu
545 550 555 560

<210> 21

<211> 521

<212> PRT

<213> Homo sapiens

<400> 21

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15

Pro	Arg	Glu	Pro	Thr	Val	Gln	Cys	Gly	Ser	Glu	Thr	Gly	Pro	Ser	Pro			
			20					25					30					
Glu	Trp	Met	Leu	Gln	His	Asp	Leu	Ile	Pro	Gly	Asp	Leu	Arg	Asp	Leu			
		35					40					45						
Arg	Val	Glu	Pro	Val	Thr	Thr	Ser	Val	Ala	Thr	Gly	Asp	Tyr	Ser	Ile			
		50				55					60							
Leu	Met	Asn	Val	Ser	Trp	Val	Leu	Arg	Ala	Asp	Ala	Ser	Ile	Arg	Leu			
		65			70					75					80			
Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser			
				85					90					95				
Tyr	Ser	Cys	Val	Arg	Cys	Asn	Tyr	Thr	Glu	Ala	Phe	Gln	Thr	Gln	Ser			
			100					105					110					
Gly	Gly	Lys	Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn			
		115					120					125						
Thr	Val	Tyr	Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn			
		130				135					140							
Glu	Asp	Gly	Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu			
		145			150					155					160			
Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu			
			165						170					175				
Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu			
			180					185					190					
Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile			
		195					200					205						
Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln			
		210				215					220							
Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser			
		225			230					235					240			
Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser			
				245					250					255				
Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly			
			260					265					270					
Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	Gly	Trp	Leu			
		275				280						285						
Pro	Ala	Ala	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro			
		290				295					300							
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe			
		305			310				315					320				
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val			
			325						330					335				
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe			
			340					345					350					

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
355 360 365

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
370 375 380

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
385 390 395 400

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
405 410 415

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
420 425 430

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
435 440 445

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
450 455 460

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
465 470 475 480

Phe Phe Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
485 490 495

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
500 505 510

Lys Ser Leu Ser Leu Ser Pro Gly Lys
515 520

<210> 22

<211> 585

<212> PRT

<213> Homo sapiens

<400> 22

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95

Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys
100 105 110

Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg
115 120 125

Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val
130 135 140

Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser
145 150 155 160

Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln
165 170 175

Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr
180 185 190

Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
195 200 205

Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile
210 215 220

Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro
225 230 235 240

Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe
245 250 255

Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser
260 265 270

Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
275 280 285

Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
290 295 300

Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
305 310 315 320

Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
325 330 335

Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Ala Ala
340 345 350

Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
355 360 365

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
370 375 380

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
385 390 395 400

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
405 410 415

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
420 425 430

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
435 440 445

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
450 455 460

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
465 470 475 480

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
485 490 495

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
500 505 510

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
515 520 525

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
530 535 540

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
545 550 555 560

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
565 570 575

Lys Ser Leu Ser Leu Ser Pro Gly Lys
580 585

<210> 23

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 23

gtacagtggc tgaccactca gaag

24

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 24

ggtggactac aagggtgaac agc

23